



SEQUENCE LISTING

<110> Hresko, Michelle Coutu
McLaird, Merry B.
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Bradley, John D.
Xu, Siqun

<120> NEMATODE PAN AND ZP RECEPTOR-LIKE
SEQUENCES

<130> 12557-015001

<140> US 10/771,708

<141> 2004-02-04

<150> US 60/444,771

<151> 2003-02-04

<160> 54

<170> FastSEQ for Windows Version 4.0

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Ile Phe Leu Ile Ser Thr Asn Ile Ala Ser Lys Ile Ser Gly Val Pro
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Thr Asn Gly Ile Leu Ala Arg Ser Leu Pro Gln Pro Gly Leu Ile Asp
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 Lys Ile Thr Asn
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 Glu His Cys Ser Ser Ser Ser Asp Cys Ile Gly Val Glu Tyr Trp Gln
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 Arg Ile Cys Ser Ser Pro Phe His Phe Asp Val Tyr Glu Gln Lys Ile
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<213> Strongyloides stercoralis

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gtt tat ttg gat aat aat tgt gct gga tcc caa tgt cat gcc cct tat Val Tyr Leu Asp Asn Asn Cys Ala Gly Ser Gln Cys His Ala Pro Tyr 210 215 220	852
gta acc caa tat gta gct gtt gaa gga aaa caa tta gct gag gaa ttg Val Thr Gln Tyr Val Ala Val Glu Gly Lys Gln Leu Ala Glu Glu Leu 225 230 235 240	900
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Ala	Ala	Pro	Pro	Pro	Ser	Val	Gln	Leu	Thr	Thr	Lys	Pro	Pro	Gln	Ile	
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cgt	gat	tta	aac	aac	aac	aat	aaa	aca	aca	cac	aaa	gaa	cca	aat	att	2148
Arg	Asp	Leu	Asn	Asn	Asn	Asn	Lys	Thr	Thr	His	Lys	Glu	Pro	Asn	Ile	
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Asp	Asp	Gly	Glu	Asn	Ser	Ile	Thr	Gly	Thr	Ala	Pro	Pro	Pro	Val	Asp	
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Val	Leu	Ile	Pro	Ala	Gln	Glu	Val	His	Thr	Ile	Cys	Asn	Tyr	Glu	Gly	
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Gly	Ser	Ser	Thr	Glu	Asp	Ile	Gln	Leu	Ile	Asn	Ser	Gln	Lys	Asp	Leu	
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Cys	Asn	Tyr	Ser	Ser	Met	Leu	Gly	Gly	Lys	Val	Gln	Thr	Ala	Ala	Ala	
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Lys	Leu	Thr	Tyr	Leu	Gln	Ala	Phe	Arg	Phe	Asp	Ser	Ser	Pro	Ala	Ile	
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cgt ttt gct att gac aat aac att aat agg aaa aat gaa gtt aaa gaa      3396
Arg Phe Ala Ile Asp Asn Asn Ile Asn Arg Lys Asn Glu Val Lys Glu
          1060                      1065                      1070

ttc gaa act cgc cgt ttt gtc gtt ccc cgt ttt gcc caa gca aca act      3444
Phe Glu Thr Arg Arg Phe Val Val Pro Arg Phe Ala Gln Ala Thr Thr
          1075                      1080                      1085

tct tta gtt att gta gac cct tta caa caa caa aat tct gtt ata aaa      3492
Ser Leu Val Ile Val Asp Pro Leu Gln Gln Gln Asn Ser Val Ile Lys
          1090                      1095                      1100

aca gaa caa caa caa caa cca ttt att tca cat tcc tca ata tct aaa      3540
Thr Glu Gln Gln Gln Gln Pro Phe Ile Ser His Ser Ser Ile Ser Lys
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Gln Ile Phe Glu Asn Asn Lys Lys Glu Asn Asn Lys Asn Ile Thr Lys
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aca gct aaa aaa tcc tct tct ctt ttt gaa gct ttt act gag gct gct      3636
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Gly Gly Arg Lys Ile Asn Leu Glu Leu Thr Thr Thr Asn Ser Glu Gln
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caa caa ctt tgt tta cat aaa tgg aca ctt ggg ggt gtt ttt gga act      3732
Gln Gln Leu Cys Leu His Lys Trp Thr Leu Gly Gly Val Phe Gly Thr
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ctt tta aca tta att gtt gtt caa agc ggg gtt gct gct aaa cat tta      3780
Leu Leu Thr Leu Ile Val Val Gln Ser Gly Val Ala Ala Lys His Leu
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Gly Phe Glu Cys Glu Ser Val Met Tyr Tyr Pro Val Asp Ala Glu Cys	
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Ile Leu Asn Thr Glu Asp Arg Leu Asp Arg Pro Asp Leu Phe Val Asp	
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Glu Cys His Trp His Phe Asp Asn Phe Lys Thr Ser Gly Ile Leu Asn	
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Gln Tyr Val Ala Val Glu Gly Arg Gln Leu Ser Asp Glu Leu Asp His	
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Ser Phe Glu Gly Leu Glu Leu Ser Glu Cys Glu Glu Leu Cys Thr Gln	
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Arg Leu Ser Val Thr Ala Asn Asp Phe Asn Cys Lys Ser Phe Met Tyr	
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Ser Arg Gly Val Pro Ser Phe Thr Arg Val Pro Gln Met Leu Leu Val	
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Gly Phe Ala Ser Phe Val Met Glu Asn Val Pro Ser Val Thr Met Cys	
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Leu Asp Gln Cys Thr Ser Pro Pro Pro Glu Thr Gly Gln Asn Phe Val
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 Met His Leu Ser
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aac cat gcc tca tca ctt ctg cat tac tat tca cat ctc atc ata att 225
 Asn His Ala Ser Ser Leu Leu His Tyr Tyr Ser His Leu Ile Ile Ile
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 Ala Tyr Phe Ser Val Phe Ala Ser Ile Glu Ile Gln Glu Ile Pro Ser
 25 30 35

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 Tyr Pro Ala Cys Ser Asn Gly Glu Ser Pro Val Phe Leu Leu Gln His
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 Thr Tyr Glu Asp Lys Glu Cys Lys Met Leu Ser Ser Ile Gly Glu Ser
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 Thr Gly His Leu Asn Asp Tyr Val Leu Leu Ser Lys Asn Cys Ala Lys
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Tyr	Ala	Pro	Tyr	Ile	Thr	Gln	Tyr	Ile	Ala	Val	Ala	Asn	Arg	Gln	Leu	
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Lys	Ser	Phe	Met	His	Asn	Pro	Glu	Thr	Asn	Val	Cys	Ile	Leu	Ser	Asp	
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Phe	Thr	Tyr	Tyr	Glu	Lys	Lys	Cys	Phe	Ala	Ser	Pro	Arg	Thr	Cys	Arg	
		295					300					305				
aat	gta	cgg	tcg	ttt	gag	cgc	ata	cct	cag	atg	ata	ctt	gtt	ggg	ttt	1137
Asn	Val	Pro	Ser	Phe	Glu	Arg	Ile	Pro	Gln	Met	Ile	Leu	Val	Gly	Phe	
		310				315					320					
gct	gca	ttt	gtt	atg	gaa	aat	gta	cct	tca	gta	acg	atg	tgc	ctc	gat	1185
Ala	Ala	Phe	Val	Met	Glu	Asn	Val	Pro	Ser	Val	Thr	Met	Cys	Leu	Asp	
325					330					335					340	
cag	tgc	aca	aat	cct	cca	ccg	gaa	act	gga	gaa	aat	ttc	gaa	tgc	aaa	1233
Gln	Cys	Thr	Asn	Pro	Pro	Pro	Glu	Thr	Gly	Glu	Asn	Phe	Glu	Cys	Lys	
				345					350					355		
tct	gtg	atg	tat	tat	tat	aac	gaa	cag	gaa	tgt	att	tta	aac	gct	gaa	1281
Ser	Val	Met	Tyr	Tyr	Tyr	Asn	Glu	Gln	Glu	Cys	Ile	Leu	Asn	Ala	Glu	

360	365	370	
aca cga gaa aat aaa tcg gaa ttg ttt ata ccg gag gga gaa gaa ttc Thr Arg Glu Asn Lys Ser Glu Leu Phe Ile Pro Glu Gly Glu Glu Phe 375 380 385			1329
caa gtc gat tat ttt gat atc act tgt cat ctg cgc cct gaa aca tgt Gln Val Asp Tyr Phe Asp Ile Thr Cys His Leu Arg Pro Glu Thr Cys 390 395 400			1377
cca aat ggc aca aca tta cat act gta cgt acg gtt aat gca gca ctc Pro Asn Gly Thr Thr Leu His Thr Val Arg Thr Val Asn Ala Ala Leu 405 410 415 420			1425
cct gaa ggc gaa gga tcg atc cat att ttg cag tca gcc ggg aat tcg Pro Glu Gly Glu Gly Ser Ile His Ile Leu Gln Ser Ala Gly Asn Ser 425 430 435			1473
gtt gct gat tgc atg aca aaa tgt tac gag atg gct ccc gag aaa tgt Val Ala Asp Cys Met Thr Lys Cys Tyr Glu Met Ala Pro Glu Lys Cys 440 445 450			1521
cgc gca ttc aat ttt gat aag cag aca tct gac tgt gac ctg ctg tac Arg Ala Phe Asn Phe Asp Lys Gln Thr Ser Asp Cys Asp Leu Leu Tyr 455 460 465			1569
gtt gat ggg aag aca acc tta cga cca gca gtc cac tcg ggc att gat Val Asp Gly Lys Thr Thr Leu Arg Pro Ala Val His Ser Gly Ile Asp 470 475 480			1617
ctc tac gac ctt cat tgc cta gag cag aca aaa gtt tgc gct cag aaa Leu Tyr Asp Leu His Cys Leu Glu Gln Thr Lys Val Cys Ala Gln Lys 485 490 495 500			1665
aac aac gta aca cga ttt tcg aga tat ttg tac agt ata tat gat gca Asn Asn Val Thr Arg Phe Ser Arg Tyr Leu Tyr Ser Ile Tyr Asp Ala 505 510 515			1713
gtg cca tcg caa ttc tac gaa gca act gcc ctc aca aat tgt ctt aat Val Pro Ser Gln Phe Tyr Glu Ala Thr Ala Leu Thr Asn Cys Leu Asn 520 525 530			1761
ctt tgc gca tat acc gag cgt tgc gaa ggt gta aat tac aac aga agg Leu Cys Ala Tyr Thr Glu Arg Cys Glu Gly Val Asn Tyr Asn Arg Arg 535 540 545			1809
aat ggt cgt tgt gaa tta ttt gat aag gtc gaa gga aat gga aag cca Asn Gly Arg Cys Glu Leu Phe Asp Lys Val Glu Gly Asn Gly Lys Pro 550 555 560			1857
agt gat ttc acg gat ttt tac aaa aat ctt tgt ctg gtg gaa gaa gta Ser Asp Phe Thr Asp Phe Tyr Lys Asn Leu Cys Leu Val Glu Glu Val 565 570 575 580			1905
gaa tca gaa tat agc gcc gca gct aat gtt ccc aaa cat ctc ctt ccg Glu Ser Glu Tyr Ser Ala Ala Ala Asn Val Pro Lys His Leu Leu Pro 585 590 595			1953

aat gtt tca cat tct gca gtt act cag aaa caa gaa gct aaa tta cac	2001
Asn Val Ser His Ser Ala Val Thr Gln Lys Gln Glu Ala Lys Leu His	
600 605 610	
att atc tca gca aaa aca aag cct ttc cta cgc gaa' cag gaa gca cag	2049
Ile Ile Ser Ala Lys Thr Lys Pro Phe Leu Arg Glu Gln Glu Ala Gln	
615 620 625	
cga cga gct cca gaa aca ata aca gcg aag tcg tct tca gct tcc gga	2097
Arg Arg Ala Pro Glu Thr Ile Thr Ala Lys Ser Ser Ser Ala Ser Gly	
630 635 640	
aaa gta agt ggt gaa gca gga tca tca act aca ttc agc att tct tca	2145
Lys Val Ser Gly Glu Ala Gly Ser Ser Thr Thr Phe Ser Ile Ser Ser	
645 650 655 660	
tcc gga agg ctt cca ggg cca gta gtc caa att gct cca aat gca gtg	2193
Ser Gly Arg Leu Pro Gly Pro Val Val Gln Ile Ala Pro Asn Ala Val	
665 670 675	
caa aca gtt tgc aat tat gaa ggc atc aaa gtg cag atg gag aac ccc	2241
Gln Thr Val Cys Asn Tyr Glu Gly Ile Lys Val Gln Met Glu Asn Pro	
680 685 690	
aaa gcc ttt tcg gga gtg ata ttt gtt aaa aat agg tat gaa acc tgt	2289
Lys Ala Phe Ser Gly Val Ile Phe Val Lys Asn Arg Tyr Glu Thr Cys	
695 700 705	
cga gta gag gtt acg gat agt gaa agt gca cca cta gta att ggt tta	2337
Arg Val Glu Val Thr Asp Ser Glu Ser Ala Pro Leu Val Ile Gly Leu	
710 715 720	
cca ccg aat ttt ggt tca aaa atg gta gct gat gaa aag gtt gcc gca	2385
Pro Pro Asn Phe Gly Ser Lys Met Val Ala Asp Glu Lys Val Ala Ala	
725 730 735 740	
agc gaa gca aat att caa cca gaa ata tcc gga ggc gac aaa ctg gat	2433
Ser Glu Ala Asn Ile Gln Pro Glu Ile Ser Gly Gly Asp Lys Leu Asp	
745 750 755	
aaa ccc gct gat gaa ctg cgc ata aga cga caa gct tta gag cta cac	2481
Lys Pro Ala Asp Glu Leu Arg Ile Arg Arg Gln Ala Leu Glu Leu His	
760 765 770	
aga gat tgc gga atc cag gat atg aac aat ggt act tat aaa tca acg	2529
Arg Asp Cys Gly Ile Gln Asp Met Asn Asn Gly Thr Tyr Lys Ser Thr	
775 780 785	
gtg gtt gta caa aca aat aac ttg ggt ata cct gga ctg gta act tcc	2577
Val Val Val Gln Thr Asn Asn Leu Gly Ile Pro Gly Leu Val Thr Ser	
790 795 800	
atg gat cag att ttt gaa gtg agc tgt gat tat agt tca atg ctt ggt	2625
Met Asp Gln Ile Phe Glu Val Ser Cys Asp Tyr Ser Ser Met Leu Gly	
805 810 815 820	

gga aaa gtt act gct ggt gcc aat ctc aca att gat ggt ccc gaa gca	2673
Gly Lys Val Thr Ala Gly Ala Asn Leu Thr Ile Asp Gly Pro Glu Ala	
825 830 835	
tct ctt att caa ccc cga gga aaa atc gaa ctt ggt aac ccg gtg ctt	2721
Ser Leu Ile Gln Pro Arg Gly Lys Ile Glu Leu Gly Asn Pro Val Leu	
840 845 850	
atg cag atg ttg agt gga caa gga gaa cct gtc cta caa gca aaa cta	2769
Met Gln Met Leu Ser Gly Gln Gly Glu Pro Val Leu Gln Ala Lys Leu	
855 860 865	
ggt gac att ctg cag cta cga tgg gaa atc atg gcg atg	2808
Gly Asp Ile Leu Gln Leu Arg Trp Glu Ile Met Ala Met	
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<210> 10

<211> 1210

<212> PRT

<213> Meloidogyne javanica

<400> 10

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20 25 30	
Ile Ser Glu Cys Asn Ser Glu Glu Ala Pro Val Phe Leu Leu Gln Arg	
35 40 45	
Asn Val Ser Ser Ile Ala Gly Thr Glu Pro Leu Arg Thr Val Pro Val	
50 55 60	
Thr Gly Gly Phe Leu Glu Cys Ala Glu Leu Cys Ser Ala Ala Asn Asn	
65 70 75 80	
Cys Val Ala Val Lys Phe Ser Ile Glu Lys Gln Cys Gln Leu Leu Gly	
85 90 95	
Lys Thr Thr Met Thr Ala Thr Thr Leu Ser Leu Gln Asp Ile Asn Leu	
100 105 110	
Thr Leu Ala Arg Leu Ala Thr Lys Ser Cys Val Lys Ser Lys Lys Ile	
115 120 125	
Cys Ser Ser Pro Phe His Phe Asp Val His Glu Gln Lys Ile Leu Val	
130 135 140	
Gly Phe Ala Arg Glu Val Val Ser Ala Glu Ser Ile His Gln Cys Leu	
145 150 155 160	
Thr Ala Cys Leu Asp Ala Val Asp Thr Phe Gly Phe Glu Cys Glu Ser	
165 170 175	
Val Met Tyr Tyr Pro Leu Asp Ala Glu Cys Ile Leu Asn Thr Glu Asp	
180 185 190	
Arg Leu Asp Arg Pro Asp Leu Phe Val Asp Glu Lys Glu Asp Thr Val	
195 200 205	
Val Tyr Leu Asp Asn Asn Cys Ala Gly Ser Gln Cys His Ala Pro Tyr	
210 215 220	
Val Thr Gln Tyr Val Ala Val Glu Gly Lys Gln Leu Ala Glu Glu Leu	
225 230 235 240	
Asp His Asn Phe Glu Gly Met Glu Leu Thr Glu Cys Glu Gln Leu Cys	
245 250 255	
Asn Gln Arg Leu Ser Val Ser Ala Asn Asp Phe Asn Cys Lys Ala Phe	
260 265 270	

Met	Tyr	Asn	Asn	Gln	Thr	Arg	Ser	Cys	Ile	Leu	Ser	Asp	Glu	Arg	Ser
		275					280					285			
Arg	Pro	Leu	Gly	Arg	Ala	Asn	Leu	Thr	Asp	Ala	Lys	Gly	Trp	Thr	Tyr
	290					295					300				
His	Glu	Lys	Lys	Cys	Phe	Ala	Ser	Pro	Arg	Thr	Cys	Arg	Asn	Val	Pro
305					310					315					320
Ser	Phe	Thr	Arg	Val	Pro	Gln	Met	Leu	Leu	Val	Gly	Phe	Ala	Ser	Phe
				325					330					335	
Val	Met	Glu	Asn	Val	Pro	Ser	Val	Thr	Met	Cys	Leu	Asp	Gln	Cys	Thr
			340					345					350		
Asn	Pro	Pro	Pro	Glu	Thr	Gly	Gln	Ser	Phe	Val	Cys	Lys	Ser	Val	Met
		355					360					365			
Tyr	Tyr	Tyr	Asn	Glu	Gln	Glu	Cys	Ile	Leu	Asn	Ala	Glu	Ser	Arg	His
	370					375					380				
Ser	Lys	Pro	Asp	Leu	Phe	Ile	Pro	Glu	Glu	Asp	Asp	Phe	Val	Val	Asp
385					390					395					400
Tyr	Phe	Asp	Ile	Asn	Cys	Arg	Leu	Glu	Gln	Glu	Gln	Cys	Ile	Asp	Gly
				405					410					415	
Arg	Thr	Pro	Gln	Leu	Val	Arg	Thr	Ile	Asn	Ser	Ala	Leu	Pro	Glu	Gly
			420					425					430		
Glu	Gly	Ser	Ile	His	Val	Leu	Glu	Thr	Ile	Lys	Gly	Gly	Val	Gln	Gln
		435					440					445			
Cys	Ala	Lys	Lys	Cys	Ser	Glu	Arg	Ala	Pro	Asp	Lys	Cys	Arg	Ser	Phe
	450					455					460				
Asn	Phe	Asp	Lys	Gln	Ala	Gly	Asn	Cys	Asn	Leu	Leu	Tyr	Leu	Asp	Gly
465					470					475					480
Gln	Gly	Ser	Leu	Arg	Pro	Glu	Gln	Lys	Thr	Gln	Phe	Asp	Leu	Tyr	Asp
				485					490					495	
Val	His	Cys	Leu	Ser	Gly	Thr	Ser	Gln	Leu	Leu	Gly	Glu	Asn	Ser	Lys
			500					505					510		
His	Ser	Pro	Ser	Ala	Cys	Val	Asp	Pro	Glu	Gly	Ala	Ile	Phe	Ser	Arg
		515					520					525			
Phe	Leu	Tyr	Thr	Arg	Trp	Val	Ala	Asn	Ser	Pro	Asn	Arg	Glu	Ile	Ser
	530					535					540				
Ser	Leu	Pro	Leu	Ser	Lys	Cys	Leu	Asn	Leu	Cys	Ser	Val	Gly	Gly	Glu
545					550					555					560
Gln	Cys	Glu	Gly	Val	Asn	Tyr	Asn	Arg	Arg	Asn	Gly	Ser	Cys	Gln	Leu
				565					570					575	
Phe	Thr	Ser	Leu	Leu	Asn	Ser	Ser	Ser	Pro	Asn	Ser	Gln	Gln	Asp	Lys
			580					585					590		
Asp	Glu	His	Val	Asp	Phe	Tyr	Arg	Asn	Ile	Cys	Arg	Val	Lys	Glu	Ser
		595					600					605			
Lys	Ser	Asp	Ser	Gly	Ala	Ala	Asn	Val	Pro	Lys	Thr	Gln	Gln	Ala	Thr
		610				615					620				
Ala	Ala	Pro	Pro												

Ile	Ser	Val	Gln	Ile	Lys	His	Ser	Ser	Pro	Phe	Ser	Gly	Val	Val	Phe	
			740					745					750			
Val	Arg	Asn	Lys	Tyr	Asp	Thr	Cys	Arg	Val	Lys	Leu	Lys	Glu	Arg	Thr	
		755					760					765				
Ala	Leu	Phe	Trp	Phe	Trp	Gly	Phe	Gln	Gln	Ile	Leu	Glu	Met	Lys	Pro	
		770				775					780					
Ile	Ala	Leu	Ile	Asn	Ser	Gln	Lys	His	Gly	Lys	Gly	Asn	Lys	Thr	His	
785					790					795					800	
Gly	Asp	Thr	Leu	Leu	Ser	Ile	Glu	Gly	Ser	Lys	Lys	Gln	Ile	Glu	Gly	
			805						810					815		
Gly	Ser	Ser	Thr	Glu	Asp	Ile	Gln	Leu	Ile	Asn	Ser	Gln	Lys	Asp	Leu	
			820					825					830			
Lys	Arg	Ser	Arg	Arg	Gln	Leu	Gln	Arg	Asp	Cys	Gly	Leu	Gln	Asp	Met	
		835					840					845				
Asp	Asn	Gly	Thr	Tyr	Lys	Thr	Val	Ile	Val	Val	Gln	Thr	Asn	Asn	Leu	
		850				855					860					
Gly	Ile	Pro	Gly	Leu	Val	Thr	Ser	Met	Asp	Gln	Leu	Tyr	Glu	Ile	Ser	
865					870					875					880	
Cys	Asn	Tyr	Ser	Ser	Met	Leu	Gly	Gly	Lys	Val	Gln	Thr	Ala	Ala	Ala	
			885						890					895		
Leu	Arg	Val	His	Gly	Pro	Gln	Pro	Ser	Leu	Ile	Gln	Pro	Arg	Gly	Lys	
			900					905					910			
Ile	Glu	Leu	Gly	Asn	Pro	Val	Leu	Met	Gln	Met	Gly	Pro	Val	Arg	Ser	
		915				920						925				
Glu	Arg	Gln	Ser	Gly	Glu	Gly	Pro	Leu	Ile	Gln	Ala	Lys	Leu	Gly	Asp	
		930				935					940					
Ile	Leu	Glu	Leu	Lys	Trp	Glu	Ile	Met	Ala	Met	Asp	Glu	Glu	Leu	Asp	
945					950					955					960	
Phe	Leu	Val	Arg	Asp	Cys	Phe	Ala	Glu	Pro	Gly	Thr	Ser	Gly	Asn	Gln	
			965						970					975		
Gly	Glu	Arg	Leu	Pro	Leu	Ile	Glu	Asn	Gly	Cys	Pro	Thr	Pro	Ala	Val	
			980					985					990			
Ala	Gln	Lys	Leu	Ile	Pro	Asn	Pro	Ile	Lys	Ala	Ile	Asn	Ser	Ala	Val	
		995					1000						1005			
Lys	Leu	Thr	Tyr	Leu	Gln	Ala	Phe	Arg	Phe	Asp	Ser	Ser	Pro	Ala	Ile	
	1010					1015						1020				
Arg	Ile	Thr	Cys	His	Leu	Glu	Leu	Cys	Lys	Glu	Asn	Cys	Lys	Ser	Val	
1025					1030					1035					1040	
Asn	Cys	Lys	Phe	Asn	Asp	Gly	Ile	Lys	Glu	Ser	Trp	Gly	Arg	Lys	Arg	
			1045						1050					1055		
Arg	Phe	Ala	Ile	Asp	Asn	Asn	Ile	Asn	Arg	Lys	Asn	Glu	Val	Lys	Glu	
			1060					1065								

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 Ile Asn Arg Phe Ile Val Gly Lys Arg Ile
 1205 1210

<210> 11
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 <212> PRT
 <213> Heterodera glycines

<400> 11
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 20 25 30
 Gly Phe Glu Cys Glu Ser Val Met Tyr Tyr Pro Val Asp Ala Glu Cys
 35 40 45
 Ile Leu Asn Thr Glu Asp Arg Leu Asp Arg Pro Asp Leu Phe Val Asp
 50 55 60
 Glu His Glu Asp Thr Val Ile Tyr Leu Asp Asn Asn Cys Ala Gly Cys
 65 70 75 80
 Glu Cys His Trp His Phe Asp Asn Phe Lys Thr Ser Gly Ile Leu Asn
 85 90 95
 Asp Gln Gln Phe Ala Ile Ala Ala Gln Cys Tyr Ala Pro Tyr Val Thr
 100 105 110
 Gln Tyr Val Ala Val Glu Gly Arg Gln Leu Ser Asp Glu Leu Asp His
 115 120 125
 Ser Phe Glu Gly Leu Glu Leu Ser Glu Cys Glu Glu Leu Cys Thr Gln
 130 135 140
 Arg Leu Ser Val Thr Ala Asn Asp Phe Asn Cys Lys Ser Phe Met Tyr
 145 150 155 160
 Ser Asn Leu Thr Arg Ser Cys Val Leu Ser Asp Glu Arg Ser Arg Pro
 165 170 175
 Leu Gly Arg Ala Asn Leu Ala Glu Val Pro Gly Trp Thr Tyr Phe Glu
 180 185 190
 Ser Arg Gly Val Pro Ser Phe Thr Arg Val Pro Gln Met Leu Leu Val
 195 200 205
 Gly Phe Ala Ser Phe Val Met Glu Asn Val Pro Ser Val Thr Met Cys
 210 215 220
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 225 230 235 240
 Cys Lys Ser Val Met Tyr Tyr Tyr Asn Glu
 245 250

<210> 12
 <211> 881
 <212> PRT
 <213> Brugia malayi

<400> 12
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 Glu Ile Pro Ser Tyr Pro Ala Cys Ser Asn Gly Glu Ser Pro Val Phe
 35 40 45
 Leu Leu Gln His Asn Ala Thr Ala Gly Asn Val Leu Lys Arg Ala Ser

50	55	60
Thr Ser His Leu Val	Asp Cys Thr Asp Leu Cys	Ser Ala Asn Asp Glu
65	70	75
Cys Leu Ala Ile Thr	Tyr Glu Asp Lys Glu Cys Lys Met Leu Ser Ser	80
85	90	95
Ile Gly Glu Ser Thr	Gly His Leu Asn Asp Tyr Val Leu Leu Ser Lys	100
100	105	110
Asn Cys Ala Lys Ser	Ala Arg Ile Cys Ser Ser Pro Phe Gln Phe Asp	115
115	120	125
Val His Arg Gln Lys	Ile Leu Val Gly Phe Ala Arg Glu Val Val Ser	130
130	135	140
Ala Asp Ser Leu Ser	Leu Cys Leu Ser Ala Cys Leu Asn Ala Phe Asp	145
145	150	155
Ser Phe Gly Phe Glu	Cys Glu Ser Val Met Tyr Tyr Pro Val Asp Ser	160
165	170	175
Glu Cys Ile Leu Asn	Thr Glu Asp Arg Leu Asp Arg Pro Asp Leu Phe	180
180	185	190
Gly Asp Glu Leu Asp	Asp Asn Val Ile Tyr Leu Asp Asn Asn Cys Ala	195
195	200	205
Gly Ser Gln Cys Tyr	Ala Pro Tyr Ile Thr Gln Tyr Ile Ala Val Ala	210
210	215	220
Asn Arg Gln Leu Ala	Asn Glu Leu Asp Arg Gln Leu Ile Ala Asp Arg	225
225	230	235
Glu Ser Cys Glu Ser	Leu Cys Thr Gln Arg Leu Ser Thr Thr Thr Asn	240
245	250	255
Asp Phe Asn Cys Lys	Ser Phe Met His Asn Pro Glu Thr Asn Val Cys	260
260	265	270
Ile Leu Ser Asp Glu	Arg Ser Lys Pro Leu Gly Arg Gly Asn Leu Val	275
275	280	285
Lys Ala Asp Gly Phe	Thr Tyr Tyr Glu Lys Lys Cys Phe Ala Ser Pro	290
290	295	300
Arg Thr Cys Arg Asn	Val Pro Ser Phe Glu Arg Ile Pro Gln Met Ile	305
305	310	315
Leu Val Gly Phe Ala	Ala Phe Val Met Glu Asn Val Pro Ser Val Thr	320
325	330	335
Met Cys Leu Asp Gln	Cys Thr Asn Pro Pro Pro Glu Thr Gly Glu Asn	340
340	345	350
Phe Glu Cys Lys Ser	Val Met Tyr Tyr Tyr Asn Glu Gln Glu Cys Ile	355
355	360	365
Leu Asn Ala Glu Thr	Arg Glu Asn Lys Ser Glu Leu Phe Ile Pro Glu	370
370	375	380
Gly Glu Glu Phe Gln	Val Asp Tyr Phe Asp Ile Thr Cys His Leu Arg	385
385	390	395
Pro Glu Thr Cys Pro	Asn Gly Thr Thr Leu His Thr Val Arg Thr Val	400
405	410	415
Asn Ala Ala Leu Pro	Glu Gly Glu Gly Ser Ile His Ile Leu Gln Ser	420
420	425	430
Ala Gly Asn Ser Val	Ala Asp Cys Met Thr Lys Cys Tyr Glu Met Ala	435
435	440	445
Pro Glu Lys Cys Arg	Ala Phe Asn Phe Asp Lys Gln Thr Ser Asp Cys	450
450	455	460
Asp Leu Leu Tyr Val	Asp Gly Lys Thr Thr Leu Arg Pro Ala Val His	465
465	470	475
Ser Gly Ile Asp Leu	Tyr Asp Leu His Cys Leu Glu Gln Thr Lys Val	480
485	490	495
Cys Ala Gln Lys Asn	Asn Val Thr Arg Phe Ser Arg Tyr Leu Tyr Ser	500
500	505	510

Ile Tyr Asp Ala Val Pro Ser Gln Phe Tyr Glu Ala Thr Ala Leu Thr
 515 520 525
 Asn Cys Leu Asn Leu Cys Ala Tyr Thr Glu Arg Cys Glu Gly Val Asn
 530 535 540
 Tyr Asn Arg Arg Asn Gly Arg Cys Glu Leu Phe Asp Lys Val Glu Gly
 545 550 555 560
 Asn Gly Lys Pro Ser Asp Phe Thr Asp Phe Tyr Lys Asn Leu Cys Leu
 565 570 575
 Val Glu Glu Val Glu Ser Glu Tyr Ser Ala Ala Ala Asn Val Pro Lys
 580 585 590
 His Leu Leu Pro Asn Val Ser His Ser Ala Val Thr Gln Lys Gln Glu
 595 600 605
 Ala Lys Leu His Ile Ile Ser Ala Lys Thr Lys Pro Phe Leu Arg Glu
 610 615 620
 Gln Glu Ala Gln Arg Arg Ala Pro Glu Thr Ile Thr Ala Lys Ser Ser
 625 630 635 640
 Ser Ala Ser Gly Lys Val Ser Gly Glu Ala Gly Ser Ser Thr Thr Phe
 645 650 655
 Ser Ile Ser Ser Ser Gly Arg Leu Pro Gly Pro Val Val Gln Ile Ala
 660 665 670
 Pro Asn Ala Val Gln Thr Val Cys Asn Tyr Glu Gly Ile Lys Val Gln
 675 680 685
 Met Glu Asn Pro Lys Ala Phe Ser Gly Val Ile Phe Val Lys Asn Arg
 690 695 700
 Tyr Glu Thr Cys Arg Val Glu Val Thr Asp Ser Glu Ser Ala Pro Leu
 705 710 715 720
 Val Ile Gly Leu Pro Asn Phe Gly Ser Lys Met Val Ala Asp Glu
 725 730 735
 Lys Val Ala Ala Ser Glu Ala Asn Ile Gln Pro Glu Ile Ser Gly Gly
 740 745 750
 Asp Lys Leu Asp Lys Pro Ala Asp Glu Leu Arg Ile Arg Arg Gln Ala
 755 760 765
 Leu Glu Leu His Arg Asp Cys Gly Ile Gln Asp Met Asn Asn Gly Thr
 770 775 780
 Tyr Lys Ser Thr Val Val Val Gln Thr Asn Asn Leu Gly Ile Pro Gly
 785 790 795 800
 Leu Val Thr Ser Met Asp Gln Ile Phe Glu Val Ser Cys Asp Tyr Ser
 805 810 815
 Ser Met Leu Gly Gly Lys Val Thr Ala Gly Ala Asn Leu Thr Ile Asp
 820 825 830
 Gly Pro Glu Ala Ser Leu Ile Gln Pro Arg Gly Lys Ile Glu Leu Gly
 835 840 845
 Asn Pro Val Leu Met Gln Met Leu Ser Gly Gln Gly Glu Pro Val Leu
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 Gln Ala Lys Leu Gly Asp Ile Leu Gln Leu Arg Trp Glu Ile Met Ala
 865 870 875 880
 Met

<210> 13

<211> 3633

<212> DNA

<213> Meloidogyne javanica

<400> 13

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60

120

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tgtgttgctg	ttaaatTTTc	tattgaaaaa	caatgccaat	tgttggggaa	aacaactatg	300
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aaaataacttg	ttggTTTTgc	tagagaagtt	gtatcagcag	aatctataca	tcaatgttta	480
actgcttggt	tagatgctgt	tgatactttt	ggctttgaat	gcgagtcagt	aatgtattat	540
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<212> PRT

<213> *Caenorhabditis elegans*

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<213> *Caenorhabditis elegans*

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Gly	Lys	Asp	Ser	Lys	Ser	Gln	Leu	Leu	Ala	Thr	Lys	Lys	Val	Lys	Lys	
	610					615					620					
Pro	Thr	Ile	Lys	Asn	Thr	Glu	His	Arg	Arg	Ala	Pro	Glu	Ser	Thr	Val	
625					630					635					640	
Pro	Ile	Gly	Pro	Pro	Val	Glu	Val	Lys	Ala	Glu	Ala	Ile	Gln	Thr	Ile	
				645					650					655		
Cys	Asn	Tyr	Glu	Gly	Ile	Lys	Val	Gln	Ile	Asn	Asn	Gly	Glu	Pro	Phe	
			660					665					670			
Ser	Gly	Val	Ile	Phe	Val	Lys	Asn	Lys	Phe	Asp	Thr	Cys	Arg	Val	Glu	
		675					680					685				
Val	Ala	Asn	Ser	Asn	Ala	Ala	Thr	Leu	Val	Leu	Gly	Leu	Pro	Lys	Asp	
	690				695						700					
Phe	Gly	Met	Arg	Pro	Ile	Ser	Leu	Asp	Asn	Ile	Asp	Asp	Asn	Glu	Thr	
705					710					715					720	
Gly	Lys	Asn	Lys	Thr	Lys	Lys	Gly	Glu	Glu	Thr	Pro	Leu	Lys	Asp	Glu	
				725					730					735		
Ile	Glu	Glu	Phe	Arg	Gln	Lys	Arg	Gln	Ala	Ala	Glu	Phe	Arg	Asp	Cys	
			740					745					750			
Gly	Leu	Val	Asp	Leu	Leu	Asn	Gly	Thr	Tyr	Lys	Ser	Thr	Val	Val	Ile	
		755					760					765				
Gln	Thr	Asn	Asn	Leu	Gly	Ile	Pro	Gly	Leu	Val	Thr	Ser	Met	Asp	Gln	
						775					780					
Leu	Tyr	Glu	Val	Ser	Cys	Asp	Tyr	Ser	Ser	Met	Leu	Gly	Gly	Arg	Val	
785					790					795					800	
Gln	Ala	Gly	Tyr	Asn	Met	Thr	Val	Thr	Gly	Pro	Glu	Ala	Asn	Leu	Ile	
				805					810					815		
Gln	Pro	Arg	Gly	Lys	Ile	Glu	Leu	Gly	Asn	Pro	Val	Leu	Met	Gln	Leu	
			820					825					830			
Leu	Asn	Gly	Asp	Gly	Thr	Glu	Gln	Pro	Leu	Val	Gln	Ala	Lys	Leu	Gly	
		835					840					845				
Asp	Ile	Leu	Glu	Leu	Arg	Trp	Glu	Ile	Met	Ala	Met	Asp	Asp	Glu	Leu	
						855										

Gly Arg Lys Lys Arg Glu Val Ser Asn Asn Ile Glu Glu Phe Glu Thr
 965 970 975
 Asn Arg Tyr Leu Ile Pro Arg Arg Ser His Ala Thr Thr Ser Ile Val
 980 985 990
 Ile Ile Asp Pro Leu Gln Gln Val Asn Glu Pro Val Ala Met Ser Arg
 995 1000 1005
 Ala Ser Thr Leu Asp Leu Leu Arg Glu Asp Ala His Glu Val Gln Met
 1010 1015 1020
 Ile Glu Glu Gly Ser Ile Cys Leu Asn Ser Val Thr Val Phe Ala Ile
 1025 1030 1035 1040
 Phe Gly Thr Leu Ala Val Leu Ile Leu Gly Gln Thr Val Val Ile Ala
 1045 1050 1055
 His Tyr Ala Val Arg Arg Phe Ser Ser Glu Lys Thr Ala
 1060 1065

<210> 18
 <211> 741
 <212> PRT
 <213> Caenorhabditis elegans

<400> 18
 Met Trp Gly Val Ile Phe Leu Leu Leu Ser Ile Val Pro Ala Ala Gln
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 Ser Val Phe Glu Cys Ser Ser His Glu Thr Thr Ala Phe Val Arg Ile
 20 25 30
 Pro Arg Ala Arg Leu Asp Gly Thr Pro Val Val Ile Ser Thr Ala Gly
 35 40 45
 His Asp Leu Thr Cys Ala Gln Tyr Cys Arg Asn Asn Ile Glu Pro Thr
 50 55 60
 Thr Gly Ala Gln Arg Val Cys Ala Ser Phe Asn Phe Asp Gly Arg Glu
 65 70 75 80
 Thr Cys Tyr Phe Phe Asp Asp Ala Ala Thr Pro Ala Gly Thr Ser Gln
 85 90 95
 Leu Thr Ala Asn Pro Ser Ala Asn Asn Phe Tyr Tyr Glu Lys Thr Cys
 100 105 110
 Ile Pro Asn Val Ser Ala His Glu Ala Cys Thr Tyr Arg Ser Phe Ser
 115 120 125
 Phe Glu Arg Ala Arg Asn Thr Gln Leu Glu Gly Phe Val Lys Lys Ser
 130 135 140
 Val Thr Val Glu Asn Arg Glu His Cys Leu Ser Ala Cys Leu Lys Glu
 145 150 155 160
 Lys Glu Phe Val Cys Lys Ser Val Asn Phe His Tyr Asp Thr Ser Leu
 165 170 175
 Cys Glu Leu Ser Val Glu Asp Lys Arg Ser Lys Pro Thr His Val Arg
 180 185 190
 Met Ser Glu Lys Ile Asp Tyr Tyr Asp Asn Asn Cys Leu Ser Arg Gln
 195 200 205
 Asn Arg Cys Gly Pro Ser Gly Gly Asn Leu Val Phe Val Lys Thr Thr
 210 215 220
 Asn Phe Glu Ile Arg Tyr Tyr Asp His Thr Gln Ser Val Glu Ala Gln
 225 230 235 240
 Glu Ser Tyr Cys Leu Gln Lys Cys Leu Asp Ser Leu Asn Thr Phe Cys
 245 250 255
 Arg Ser Val Glu Phe Asn Pro Lys Glu Lys Asn Cys Ile Val Ser Asp
 260 265 270
 Glu Asp Thr Phe Ser Arg Ala Asp Gln Gln Gly Gln Val Val Gly Lys
 275 280 285

Asp	Tyr	Tyr	Glu	Pro	Ile	Cys	Val	Ala	Ala	Asp	Leu	Ser	Ser	Ser	Thr
290						295					300				
Cys	Arg	Gln	Gln	Ala	Ala	Phe	Glu	Arg	Phe	Ile	Gly	Ser	Ser	Ile	Glu
305					310					315					320
Gly	Glu	Val	Val	Ala	Ser	Ala	Gln	Gly	Val	Thr	Ile	Ser	Asp	Cys	Ile
				325					330					335	
Ser	Leu	Cys	Phe	Gln	Asn	Leu	Asn	Cys	Lys	Ser	Ile	Asn	Tyr	Asp	Arg
			340					345					350		
Thr	Ala	Ser	Ser	Cys	Phe	Ile	Tyr	Ala	Val	Gly	Arg	Gln	Asp	Ala	Asn
		355					360						365		
Ile	Lys	Ala	Asn	Pro	Ser	Met	Asp	Tyr	Tyr	Glu	Phe	Asn	Cys	Glu	Ser
	370					375					380				
Gln	Phe	Gly	Gly	Met	Ala	Leu	Cys	Thr	Asn	Glu	Gly	Ile	Arg	Phe	Ile
385					390					395					400
Val	Asn	Thr	Lys	Glu	Pro	Tyr	Thr	Gly	Ala	Ile	Tyr	Ala	Ala	Glu	Arg
				405					410					415	
Phe	Ser	Thr	Cys	Ser	Gln	Val	Val	Glu	Asn	Ala	Lys	Gln	Ile	Ser	Ile
			420					425					430		
Thr	Phe	Pro	Pro	Pro	Thr	Val	Ser	Ser	Asp	Cys	Gly	Thr	Val	Ile	Arg
		435					440					445			
Asp	Gly	Lys	Met	Glu	Ala	Leu	Val	Val	Val	Ser	Leu	Asp	Gly	Val	Leu
	450					455					460				
Pro	His	Gln	Val	Thr	Thr	Glu	Trp	Asp	Arg	Phe	Tyr	Arg	Val	Ser	Cys
465					470					475					480
Asp	Val	Ser	Met	Asp	Lys	Met	Val	Lys	Glu	Gly	Ser	Val	Val	Val	Thr
				485					490					495	
Thr	Ile	Tyr	Glu	Ala	Ser	Ser	Gln	Asn	Thr	Thr	Val	Leu	Asp	Val	Ala
			500					505					510		
Thr	Pro	Pro	Pro	Val	Ser	Ala	Glu	Leu	Gln	Ile	Leu	Asn	Gln	Leu	Glu
		515					520					525			
Glu	Pro	Leu	His	Lys	Ala	Ser	Ile	Gly	Asp	Pro	Leu	Leu	Leu	Val	Ile
	530					535					540				
Thr	Ser	Glu	Gln	Ala	Gly	Pro	His	Asn	Met	Met	Val	Thr	Glu	Cys	Thr
545					550					555					560
Ala	Thr	Arg	Val	Gly	Gly	Phe	Gly	Asp	Thr	Val	Pro	Phe	Thr	Leu	Ile
				565					570					575	
Glu	Asn	Gly	Cys	Pro	Arg	Tyr	Pro	Ala	Leu	Val	Gly	Pro	Val	Glu	Gln
			580					585					590		
Asp	Phe	Asp	Lys	Asn	Arg	Leu	Lys	Ser	Asp	Leu	Arg	Ala	Phe	Arg	Leu
		595					600					605			
Asp	Gly	Ser	Tyr	Asp	Val	Gln	Ile	Val	Cys	Ser	Ile	Met	Phe	Cys	Ala
	610					615					620				
Gly	Pro	Asn	Gly	Cys	Pro	Val	Ser	Asn	Cys	Leu	Asp	Ser	Gly	Thr	Asn
625					630					635					640
Glu	Leu	Phe	Met	S											

740

<210> 19
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 19
 ggccacgcgt cgactagtac 20

<210> 20
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 20
 gggttttaatt acccaagttt ga 22

<210> 21
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 21
 ggccacgcgt cgactagtac tttttttttt ttttttt 37

<210> 22
 <211> 44
 <212> RNA
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<220>
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<400> 22
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<210> 23
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<220>
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<400> 23
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<210> 24
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<220>
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<400> 24
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<220>
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<400> 25
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<210> 26
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<220>
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<400> 26
 ggacactgac atggactgaa ggagta 26

<210> 27
 <211> 20
 <212> DNA
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<220>
 <223> Primer

<400> 27
 tcagtgcgct tatgtcctcc 20

<210> 28
 <211> 20
 <212> DNA
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<220>
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<400> 28
 tgacagatgg aacattctcc 20

<210> 29
 <211> 20

<212> DNA
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<220>
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<400> 29
 acttcaggac acgacttgac 20

<210> 30
 <211> 20
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<220>
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<400> 30
 caatcagaga tggtaactcc 20

<210> 31
 <211> 26
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<220>
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<400> 31
 cgttgtagac agtcgctgag tacata 26

<210> 32
 <211> 22
 <212> DNA
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<220>
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<400> 32
 ccaactcggt agctagctga cg 22

<210> 33
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 33
 cgaacatgtc gcaatgtac 19

<210> 34
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<221> misc_feature

<222> 4

<223> n = a, t, c, or g

<400> 34

catngccatd atytccca

18

<210> 35

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<221> misc_feature

<222> 6

<223> n = a, t, c, or g

<400> 35

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18

<210> 36

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 36

gatcgaggca catcgttac

19

<210> 37

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 37

gttttagatgc tgttgatac

19

<210> 38

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<221> misc_feature

<222> 9, 15
 <223> n = a, t, c, or g

<400> 38
 tcdatyttnc cyctnggytg 20

<210> 39
 <211> 20
 <212> DNA
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<220>
 <223> Primer

<400> 39
 caagatatgg acaatggaac 20

<210> 40
 <211> 20
 <212> DNA
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<220>
 <223> Primer

<400> 40
 atacattcgg catccaatgg 20

<210> 41
 <211> 20
 <212> DNA
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<220>
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<400> 41
 actgactcgc attcaaagcc 20

<210> 42
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<220>
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<400> 42
 tagctaattct agctagtgtc 20

<210> 43
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 <212> DNA
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<220>
 <223> Primer

<221> misc_feature
 <222> 15
 <223> n = a, t, c, or g

<400> 43
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17

<210> 44
 <211> 20
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 <213> Artificial Sequence

<220>
 <223> Primer

<400> 44
 tgytcrtrtrt artartacat

20

<210> 45
 <211> 1068
 <212> PRT
 <213> Caenorhabditis briggsae

<400> 45
 Met Lys Val Phe Ala Val Val Ala Leu Leu Ala Val Ser Ala Leu Ala
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 Asp Thr Leu Pro Ser Val Thr Ile Cys Pro Pro Glu Thr Gln Thr Ile
 20 25 30
 Phe Val Leu Gln His Asn Ser Thr Val Gly Ala Arg Ile Arg Thr Ile
 35 40 45
 Pro Thr Ser Asn Leu Ala Glu Cys Ser Asp His Cys Ala Ala Ser Leu
 50 55 60
 Asp Cys Gln Gly Val Glu Phe Lys Asp Gly Ser Cys Ala Val Phe Arg
 65 70 75 80
 Ala Gly Ser Glu Lys Ala Thr Lys Gly Ser Gln Leu Leu Thr Lys Ser
 85 90 95
 Cys Val Lys Ser Asp Arg Val Cys Gln Ser Pro Phe Gln Phe Asp Leu
 100 105 110
 Phe Glu Gln Lys Ile Leu Val Gly Phe Ala Arg Glu Val Val Pro Ala
 115 120 125
 Glu Asn Ile Gln Val Cys Met Ala Ala Cys Leu Asn Ala Phe Asp Thr
 130 135 140
 Phe Gly Phe Glu Cys Glu Ser Ala Met Phe Tyr Pro Val Asp Gln Glu
 145 150 155 160
 Cys Ile Leu Asn Thr Glu Asp Arg Leu Asp Arg Pro Ser Leu Phe Val
 165 170 175
 Asp Glu Ala Asp Asp Thr Val Ile Tyr Met Asp Asn Asn Cys Ala Gly
 180 185 190
 Cys Lys Phe Gln Asn Pro Cys Ser His Val Asp Leu Tyr Phe Ser Leu
 195 200 205
 Ala Gln Cys Tyr Pro Pro Tyr Ile Thr Gln Tyr Ile Ala Val Glu Gly
 210 215 220
 Lys Gln Leu Lys Asn Glu Leu Asp Arg Ile Ile Asn Val Asp Leu Asp
 225 230 235 240
 Ser Cys Gln Ala Leu Cys Thr Gln Arg Leu Ser Ile Ser Ser Asn Asp
 245 250 255

Phe	Asn	Cys	Lys	Ser	Phe	Met	Tyr	Asn	Asn	Lys	Thr	Arg	Thr	Cys	Ile	260	265	270
Leu	Ala	Asp	Glu	Arg	Ser	Lys	Pro	Leu	Gly	Arg	Ala	Asp	Leu	Val	Ala	275	280	285
Thr	Glu	Gly	Phe	Thr	Tyr	Phe	Glu	Lys	Lys	Cys	Phe	Ala	Ser	Pro	Asn	290	295	300
Thr	Cys	Arg	Asn	Val	Pro	Ser	Phe	Lys	Arg	Val	Pro	Gln	Met	Ile	Leu	305	310	315
Val	Gly	Phe	Ala	Ala	Phe	Val	Met	Glu	Asn	Val	Pro	Ser	Val	Thr	Met	320	325	330
Cys	Leu	Asp	Gln	Cys	Thr	Asn	Pro	Pro	Pro	Glu	Thr	Gly	Asp	Gly	Phe	335	340	345
Val	Cys	Lys	Ser	Val	Met	Tyr	Tyr	Tyr	Asn	Glu	Gln	Glu	Cys	Ile	Leu	350	355	360
Asn	Ser	Glu	Thr	Arg	Glu	Ser	Lys	Pro	Glu	Leu	Phe	Ile	Pro	Glu	Gly	365	370	375
Glu	Glu	Phe	Leu	Val	Asp	Tyr	Phe	Asp	Ile	Thr	Cys	His	Leu	Lys	Gln	380	385	390
Glu	Lys	Cys	Pro	Ala	Gly	Gln	His	Leu	Lys	Ala	Ile	Arg	Thr	Ile	Asn	395	400	405
Ala	Ala	Leu	Pro	Glu	Gly	Glu	Ser	Glu	Leu	His	Val	Leu	Lys	Ser	Ser	410	415	420
Ala	Ala	Lys	Gly	Ile	Lys	Glu	Cys	Val	Ala	Lys	Cys	Phe	Gly	Leu	Ala	425	430	435
Pro	Glu	Lys	Cys	Arg	Ser	Phe	Asn	Tyr	Asp	Lys	Lys	Thr	Lys	Ser	Cys	440	445	450
Asp	Leu	Leu	Tyr	Leu	Asp	Gly	His	Asn	Thr	Leu	Gln	Pro	Gln	Val	Arg	455	460	465
Gln	Gly	Val	Asp	Leu	Tyr	Asp	Leu	His	Cys	Leu	Ala	Ala	Leu	Pro	Leu	470	475	480
Val	Glu	Asn	Asp	Cys	Ser	Ala	Asn	Lys	Asp	Asp	Ala	Leu	Phe	Ser	Arg	485	490	495
Tyr	Leu	His	Thr	Lys	Gln	Arg	Gly	Ile	Pro	Ala	Lys	Ser	Tyr	Lys	Val	500	505	510
Val	Ser	Leu	Asn	Ser	Cys	Leu	Glu	Val	Cys	Ala	Gly	Asn	Pro	Thr	Cys	515	520	525
Ala	Gly	Ala	Asn	Tyr	Asn	Arg	Arg	Leu	Gly	Asp	Cys	Ser	Leu	Phe	Asp	530	535	540
Ala	Ile	Asp	Lys	Asp	Ala	Glu	Val	Asn	Glu	His	Thr	Asp	Phe	Tyr	Lys	545	550	555
Asn	Leu	Cys	Val	Thr	Lys	Glu	Val	Asp	Thr	Gly	Ala	Ser	Ala	Ala	Ala	560	565	570
Asn	Val	Pro	Glu	Thr	Lys	His	Arg	Val	Ser	Gly	Thr	Val	Val	Glu	Gly	575	580	585
Lys	Asp	Ser	Lys	Ala	Gln	Leu	Leu	Ala	Thr	Lys	Lys	Val	Lys	Lys	Pro	590	595	600
Thr	Ile	Lys	Asn	Thr	Glu	His	Arg	Arg	Ala	Pro	Glu	Ser	Thr	Val	Pro	605	610	615
Leu	Gly	Pro	Pro	Val	Glu	Val	Lys	Ala	Glu	Ala	Ile	Gln	Thr	Ile	Cys	620	625	630
Asn	Tyr	Glu	Gly	Ile	Lys	Val	Gln	Ile	Asn	Asn	Gly	Glu	Pro	Phe	Ser	635	640	645
Gly	Val	Ile	Phe	Val	Lys	Asn	Lys	Phe	Asp	Thr	Cys	Arg	Val	Glu	Val	650	655	660
Ala	Asn	Ser	Asn	Ala	Ala	Thr	Leu	Val	Leu	Gly	Leu	Pro	Lys	Asp	Phe	665	670	675
Gly	Met	Arg	Pro	Ile	Ser	Leu	Asp	Asn	Leu	Asp	Asp	Asn	Glu	Thr	Gly	680	685	690

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705          710          715          720
Lys Asn Lys Thr Lys Lys Gly Glu Glu Thr Pro Leu Lys Glu Glu Ile
          725          730          735
Glu Glu Phe Arg Gln Lys Arg Gln Ala Ala Glu Phe Arg Asp Cys Gly
          740          745          750
Leu Val Asp Leu Leu Asn Gly Thr Tyr Lys Ser Thr Val Val Ile Gln
          755          760          765
Thr Asn Asn Leu Gly Ile Pro Gly Leu Val Thr Ser Met Asp Gln Leu
          770          775          780
Tyr Glu Val Ser Cys Asp Tyr Ser Ser Met Leu Gly Gly Arg Val Gln
785          790          795          800
Ala Gly Tyr Asn Met Thr Val Thr Gly Pro Glu Ala Asn Leu Ile Gln
          805          810          815
Pro Arg Gly Lys Ile Glu Leu Gly Asn Pro Val Leu Met Gln Leu Leu
          820          825          830
Asn Gly Asp Gly Thr Glu Gln Pro Leu Val Gln Ala Lys Leu Gly Asp
          835          840          845
Ile Leu Glu Leu Arg Trp Glu Ile Met Ala Met Asp Asp Glu Leu Asp
          850          855          860
Phe Phe Val Lys Asn Cys His Ala Glu Pro Gly Leu Ala Gly Gly Lys
865          870          875          880
Ala Gly Ala Gly Glu Lys Leu Gln Leu Ile Asp Gly Gly Cys Pro Thr
          885          890          895
Pro Ala Val Ala Gln Lys Leu Ile Pro Gly Ala Ile Glu Val Lys Ser
          900          905          910
Ser Ala Val Lys Thr Thr Lys Met Gln Ala Phe Arg Phe Asp Ser Ser
          915          920          925
Ala Ser Ile Arg Val Thr Cys Glu Val Glu Ile Cys Lys Gly Asp Cys
          930          935          940
Glu Ala Val Glu Cys Ala Leu Thr Gly Gly Val Lys Lys Ser Phe Gly
945          950          955          960
Arg Lys Lys Arg Glu Val Asn Asn Asn Ile Glu Glu Phe Glu Thr Asn
          965          970          975
Arg Tyr Leu Ile Pro Arg Arg Ser His Ala Thr Thr Ser Ile Val Ile
          980          985          990
Ile Asp Pro Leu Gln Gln Val Asn Glu Pro Val Ala Met Ser Arg Ala
          995          1000          1005
Ser Thr Leu Asp Leu Leu Arg Glu Glu Ala His Glu Val Gln Val Ile
          1010          1015          1020
Glu Glu Gly Ser Ile Cys Leu Asn Arg Ile Thr Val Phe Ala Ile Phe
1025          1030          1035          1040
Gly Thr Leu Ala Val Leu Ile Leu Gly Gln Val Ile Val Val Ala His
          1045          1050          1055
Tyr Ala Val Arg Arg Phe Ser Thr Glu Lys Thr Ala
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<210> 46

<211> 742

<212> PRT

<213> Caenorhabditis briggsae

<400> 46

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Met Ser Pro Arg Val Ile Phe Leu Leu Leu Gly Ser Phe Leu Thr Ala
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Gln Ala Val Phe Glu Cys Ser Ser His Glu Thr Thr Ala Phe Val Arg
          20          25          30
Ile Pro Arg Ala Arg Leu Asp Gly Thr Pro Val Val Ile Ser Thr Ala

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		35				40				45					
Gly	His	Asp	Leu	Thr	Cys	Ala	Gln	Tyr	Cys	Arg	Asn	Asn	Ile	Glu	Pro
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Thr	Thr	Gly	Ala	Gln	Arg	Val	Cys	Ala	Ser	Phe	Asn	Phe	Asp	Gly	Arg
65					70					75					80
Glu	Thr	Cys	Tyr	Phe	Phe	Asp	Asp	Ala	Ala	Thr	Pro	Ala	Gly	Thr	Ser
				85					90					95	
Gln	Leu	Thr	Ala	Asn	Pro	Ser	Ala	Asn	Asn	Phe	Tyr	Tyr	Glu	Lys	Thr
			100					105					110		
Cys	Ile	Pro	Asn	Val	Ser	Ala	His	Glu	Ala	Cys	Thr	Tyr	Arg	Ser	Phe
			115				120					125			
Ser	Phe	Glu	Arg	Ala	Arg	Asn	Thr	Gln	Leu	Glu	Gly	Phe	Val	Lys	Lys
	130					135					140				
Ser	Val	Thr	Val	Lys	Asn	Arg	Glu	His	Cys	Leu	Ser	Ala	Cys	Leu	Lys
145					150					155					160
Glu	Lys	Glu	Phe	Val	Cys	Lys	Ser	Val	Asn	Phe	His	Tyr	Glu	Asn	Ser
				165					170					175	
Leu	Cys	Glu	Leu	Ser	Val	Glu	Asp	Lys	Arg	Ser	Lys	Pro	Thr	His	Val
			180					185					190		
Arg	Met	Ser	Glu	Gly	Ile	Asp	Tyr	Tyr	Asp	Asn	Asn	Cys	Leu	Ser	Arg
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Gln	Asn	Arg	Cys	Gly	Pro	Ser	Gly	Gly	Asn	Leu	Val	Phe	Val	Lys	Thr
	210					215					220				
Thr	Asn	Phe	Glu	Ile	Arg	Tyr	Tyr	Asp	His	Thr	Gln	Ser	Val	Glu	Ala
225					230					235					240
Gln	Glu	Ser	Tyr	Cys	Leu	Gln	Lys	Cys	Leu	Asp	Ser	Leu	Asn	Thr	Phe
				245					250					255	
Cys	Arg	Ser	Val	Glu	Phe	Asn	Pro	Lys	Glu	Lys	Asn	Cys	Ile	Val	Ser
			260					265					270		
Asp	Glu	Asp	Thr	Phe	Ser	Arg	Ala	Asp	Gln	Gln	Gly	Gln	Val	Val	Gly
		275					280					285			
Lys	Asp	Tyr	Tyr	Glu	Pro	Ile	Cys	Val	Ala	Ala	Asp	Leu	Ser	Ser	Ser
	290					295					300				
Thr	Cys	Arg	Gln	Gln	Ala	Ala	Phe	Glu	Arg	Phe	Ile	Gly	Ser	Ser	Ile
305					310					315					320
Glu	Gly	Glu	Val	Val	Ala	Ser	Ala	Gln	Gly	Val	Thr	Ile	Ser	Asp	Cys
				325					330					335	
Ile	Ser	Leu	Cys	Phe	Gln	Asn	Leu	Asn	Cys	Lys	Ser	Ile	Asn	Tyr	Asp
			340					345					350		
Arg	Thr	Ala	Ser	Ser	Cys	Phe	Ile	Tyr	Ala	Val	Gly	Arg	Gln	Asp	Ala
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Cys	Asp	Val	Ser	Met	Asp	Lys	Met	Val	Lys	Glu	Gly	Ser	Val	Val	Val
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 Glu Glu Pro Leu His Lys Ala Ser Ile Gly Asp Pro Leu Leu Leu Val
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 Leu Asp Gly Ser Tyr Asp Val Gln Ile Val Cys Ser Ile Met Phe Cys
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 Ala Gly Pro Asn Gly Cys Pro Val Ser Asn Cys Leu Asp Ser Gly Thr
 625 630 635 640
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 Glu Ala Gly Glu Thr Glu Glu Arg Leu Ser Ala Ile Ile Arg Val Phe
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 Ala Lys Gly Glu Asp Glu Glu Glu Ile Glu Met Gly Asn Asn Thr Leu
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 Met Thr Ser Leu Ala Glu Ser Thr Asp Leu Leu Cys Ile Ala Glu Pro
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